

1/19

FIG. 1

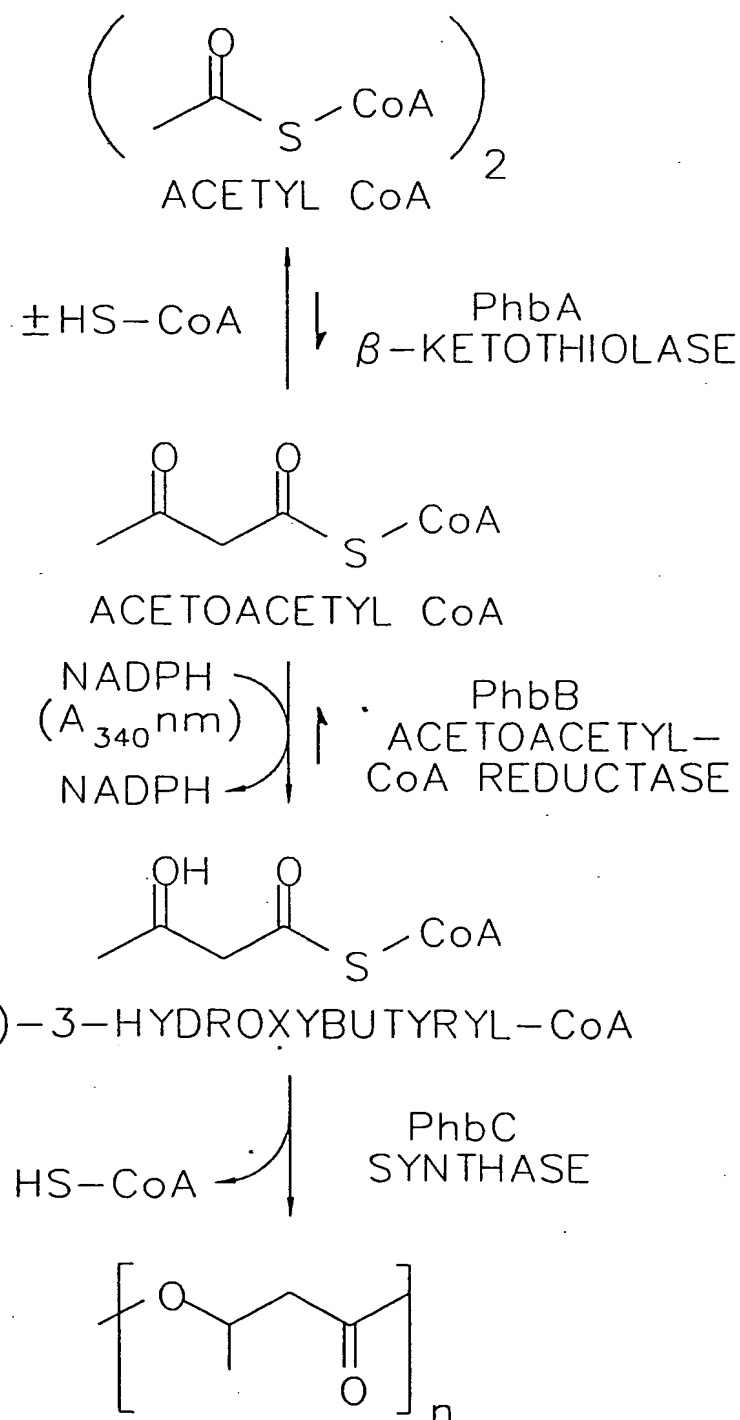
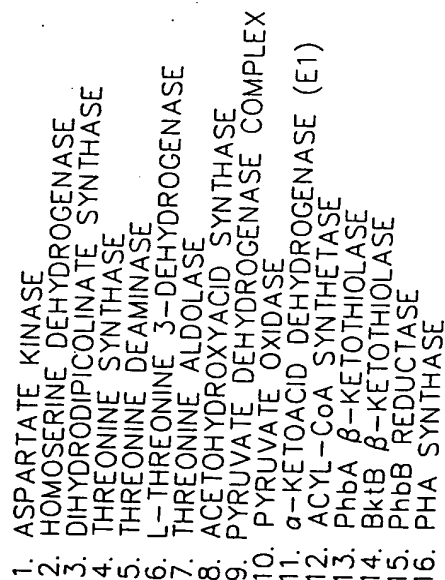


FIG. 3



4/19

FIG. 4

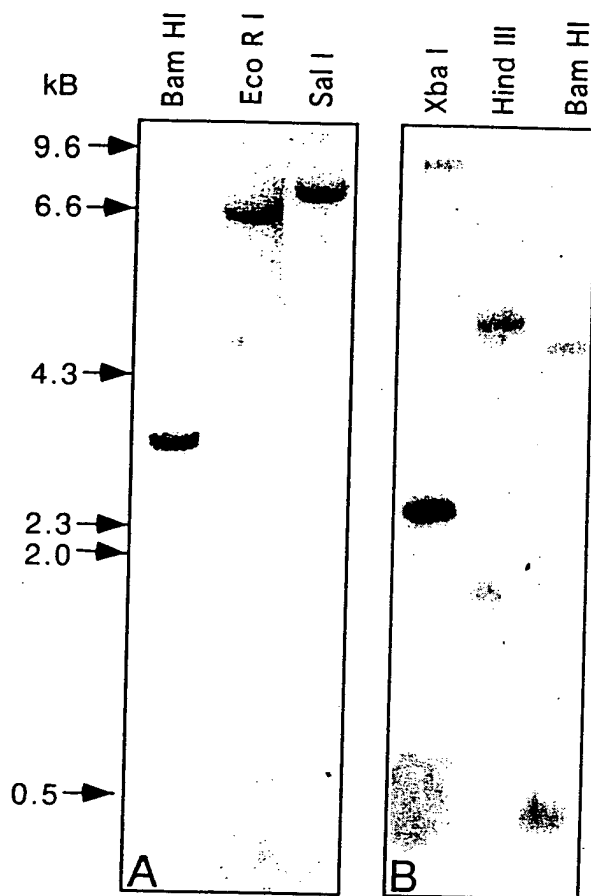
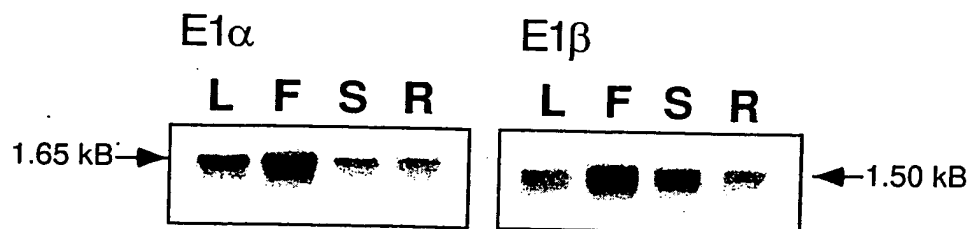


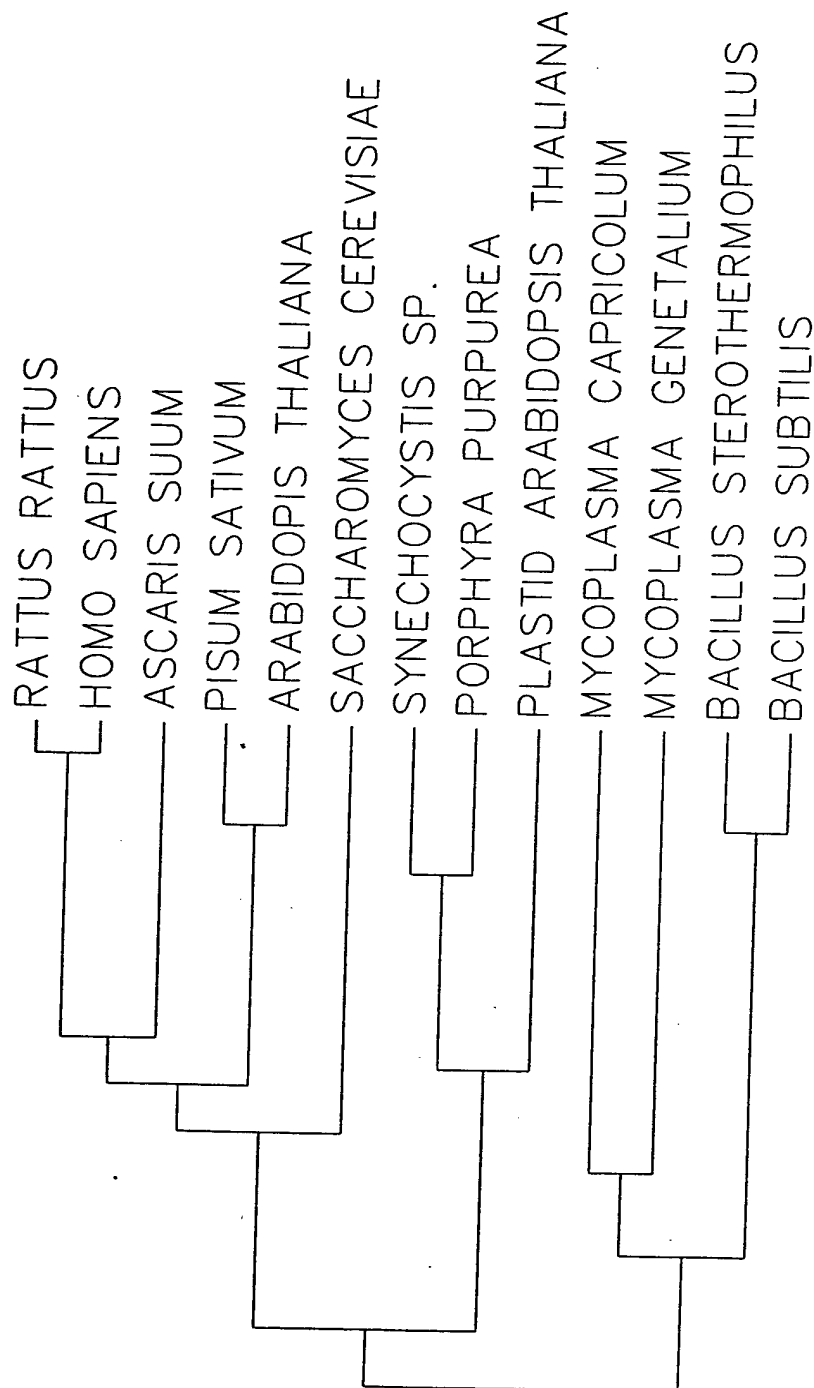
FIG. 5



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5/19

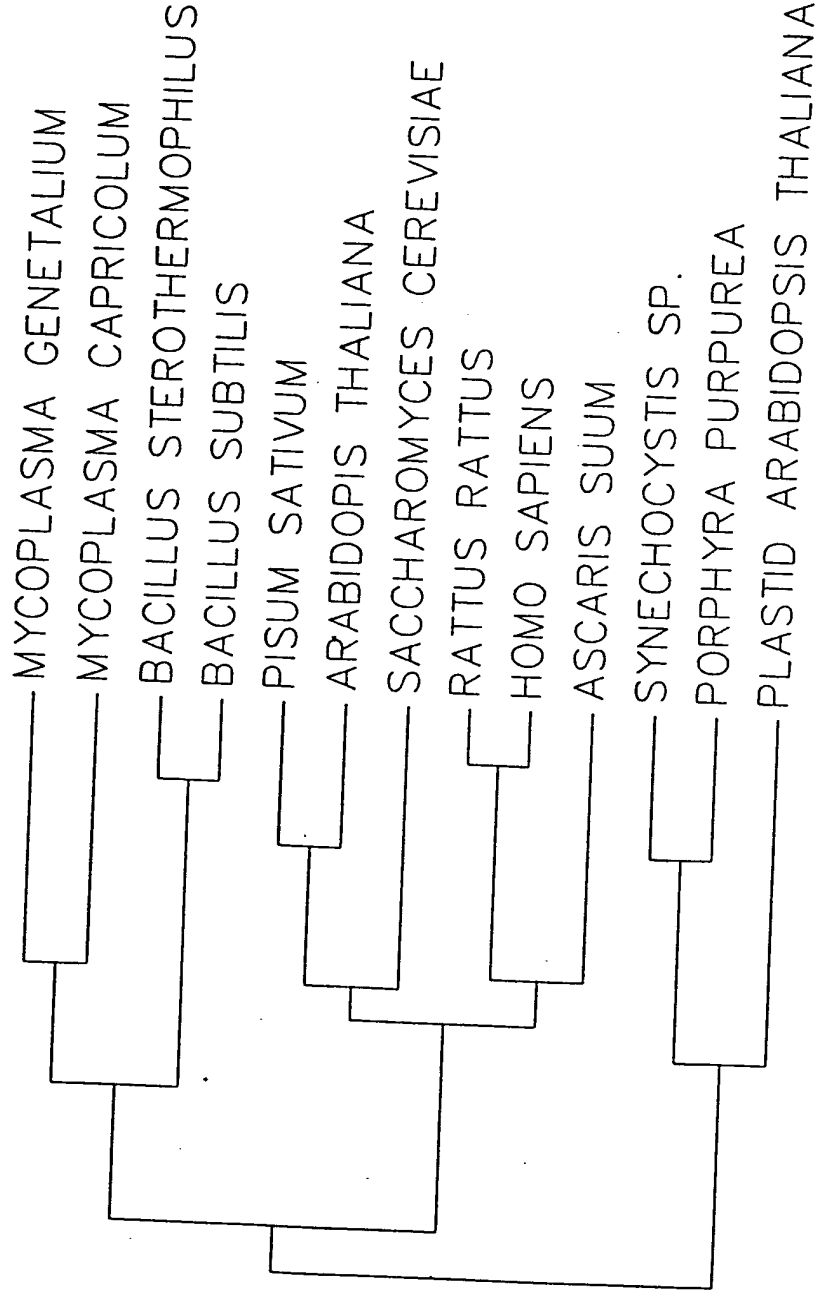
FIG. 6A



6/19

6/19/66

FIG. 6B



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9/19

FIG. 7C

BRANCHED-CHAIN E2



PLASTID E2



PLASTID TARGETED BRANCHED-CHAIN E2

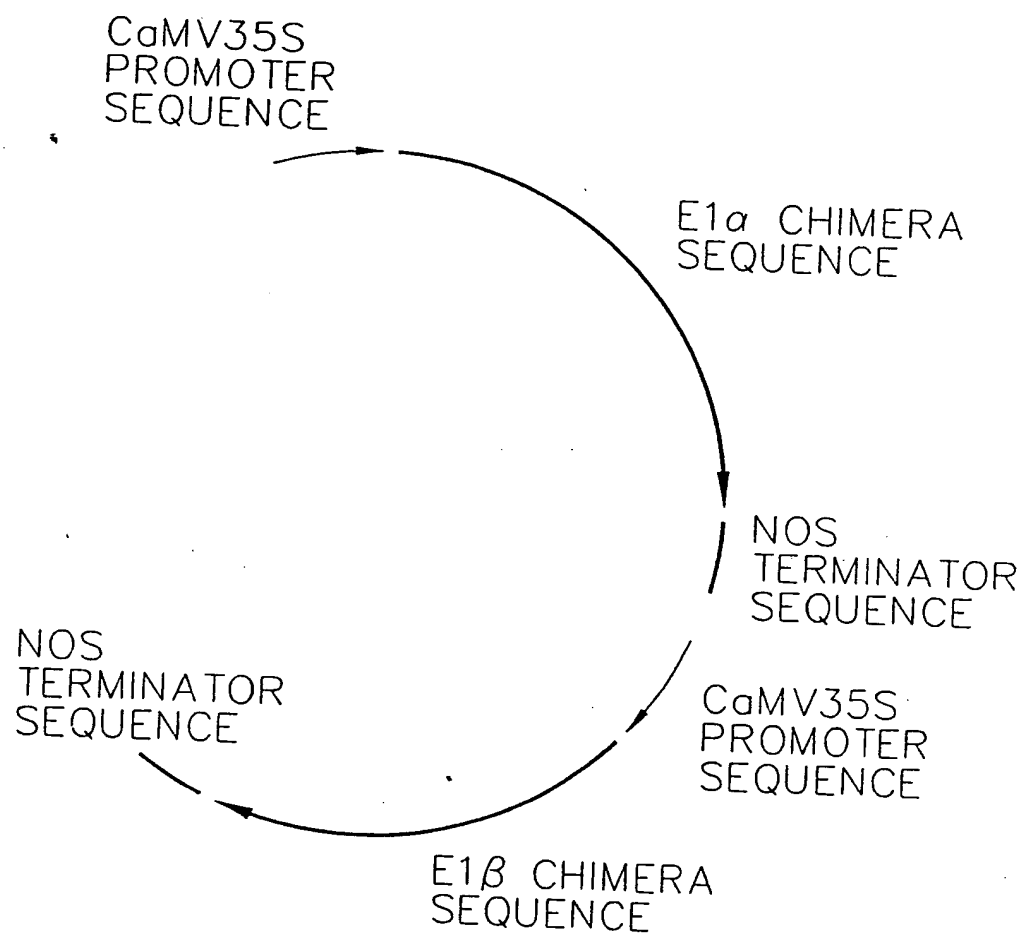


CONSTRUCT 3: ATTACH THE CHLOROPLAST TARGETING PEPTIDE OF THE PLASTID E2 TO THE MATURE PORTION OF THE BRANCHED-CHAIN E2, TO CREATE A PLASTID TARGETED BRANCHED-CHAIN E2 CHIMERA.

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10/19

FIG. 7D

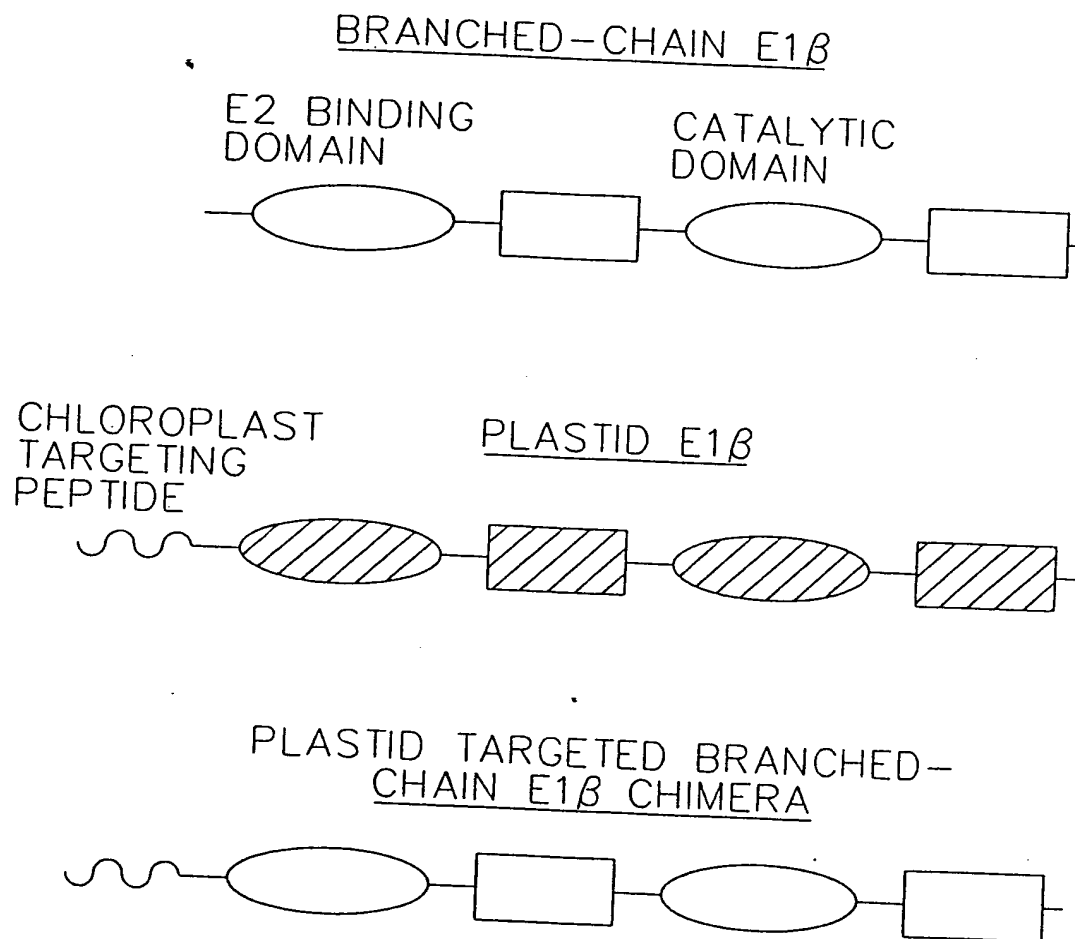


CONSTRUCT 4: MEGA PLASMID CODING FOR BOTH CHIMERIC (PLASTID TARGETED BRANCHED-CHAIN) SUBUNITS OF THE PDH. ATTACH THE E1 α CHIMERIC SEQUENCE TO THE E1 β CHIMERIC SEQUENCE WITH TRANSCRIPTION TERMINATOR AND PROMOTER SEQUENCES BETWEEN THE TWO.

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11/19

FIG. 7E



CONSTRUCT 5: ATTACH THE CHLOROPLAST TARGETING PEPTIDE OF THE PLASTID E1 β TO THE MATURE PORTION OF THE BRANCHED-CHAIN E1 β . THIS CREATES A PLASTID TARGETED BRANCHED-CHAIN E1 β CHIMERA.

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12/19

FIG. 8A

Plastid A.t.	MATAFAPTKLTATVPLHGSHENRLLLPIRLAPPSSFLGSTRSLSLRRLNH	50
<i>P.purpurea</i>	-----	
<i>A.thaliana</i>	-----MALSRSSRSNIITRPFSAAFSRLIS	26
<i>H.sapiens</i> II	-----MRKMLAAVSRVLSGASQKPASRVLVAS	27
<i>S.cerevisiae</i>	---MLAASFQRQPSQLVRGLGAVLRTPTRIGHVRTMATLKTDDKAPEDI	47
<i>A.suum</i> I	-----MIFVFANIFKVPTVSPSVMAISV	23
<i>M.capricolum</i>	-----MTYL	4
<i>B.subtilis</i>	-----MGVKTFFQFPFAEQL	14
Consensus	-----	50

Motif 1

SNATRRSPVVSQEVVKEQSTNNTSLITKEEGLELYEDMILGRSFEDM	100
-----MSYPKKVELPLTNCNQINLTCHKLLVLYEDMLLGRNFEDM	40
TDTTPITIETSLPFTAHLCDPPSRVSESSQELLD-FFRTMALMRRMEIA	75
RNFANDATFEIKKCDLHRLEEGPPVTTVLTREDGLKYRMMQTVRRMELK	77
EGSDTVQIELPESSFESYMLEPPDLSYETSKATLLQMYKDMVIRRMEMA	97
RLASTEATFQTKPFKLHKLDSPDINVHVTKEDAVHYTQMLTIRRMESA	73
GKFDPLKNEKVCVLDKDGKVINPKLMPKISDQEIIEAYKIMNLSRRQDIY	54
EKVAEQFPFTFQILNEEGEVVNEEAMPFELSDEQLKE-LMRRMVYTRILDQR	63
.....L..Y..M...RR.E..	100

o

CAQMYRGRKMGFVHLYNGQEAVSTGFIKLLTKSDSVVSTYRDHVALSK	150
CAQMYRGRKMGFVHLYNGQEAVSTGVIKLLSKDYVCSTYRDHVALSK	90
ADSLYKANVIRGFCHLYDGQEAVAIGMEAAITKKDAIITAYRDHCFILGR	125
ADQLYKQKIIRGFCHLCDGQEACCVGLEAGINPTDHLITAYRAHGFTFTR	127
CDALYKAKKIRGFCHLSVGQEAIAVGIEAITKLDISIITSYRCHGFTFMR	147
AGNLYKEKKVRGFCHLYSGQEACAVGTKAAMDAGDAAVTAYRCHGWYLS	123
QNTMQRQGRLLSFLSSTGQEACEVAYINALNKKTDHFVSGYRNNAAWLAM	104
SISLNRQGRG-LGYAPTAGEASQIASHFALEKEDFILPGYRDVPQIIWH	112
...LY.....GF.HL..GQEA...G.....K.D.....YR.H.....	150

13/19

FIG. 8B

TPP-binding site

GVSARAVMSELFVKVTGCCRGQGGSMHMFKEHNMLGGFAFIGEGIPVAT	200
GVPSONVMAELFGKETGCSRGRGGSMHIFSAFHNFLGGFAFIAEGIPVAT	140
GGSLHEVFSSELMGRQAGCSKGKGGSMHIFYKKESSFYGGHGIVGAQVPLGC	175
GLSVREILAEALTGRKGGCAKGGKGGSMHMYAKN--FYGGNGIVGAQVPLGA	175
GASVRAVLAELMGRRAGVSYGKGGSMHLYAPG--FYGGNGIVGAQVPLGA	195
GSSVAKVLCALTGRITGNVYGGKGGSMHMYGEN--FYGGNGIVGAQVPLGT	171
GQLVRNIMLYWIGNEAG-GKAPEG-VNCLPPN-----IVIGSQYSQAT	145
GLPLYQAFLFSRGHFHG-NQIPEG-VNVLPPQ-----IIIGAQYIQAA	153

G.S...V..EL.G...G...G.GGSMH.....-F.GG..I.GAQ.P...	200
---	-----

PDH β binding site

GAAFSSKYRREVLKQDCD-DVTVAFFGDGTCNNGQFFECNLMAALYKLPI	249
GAAFQSIYRQQLKEPGLRVTACFFGDGTTNNGQFFECNLMAVLWKLPI	190
GIAFAQKYNKE---EA---VTFALYGDGAANQGQLFEALNISALWDLPA	218
GIALACKYNGK---DE---VCLTLYGDGAANQGQIFEAYNMAALWKLPC	218
GLAFAHQYKNE---DA---CSFTLYGDGASNQGQVFESFNMAKLWNLV	238
GIAFAMKYRKE---KN---VCITMFGDGATNQGQLFESMNMAKLWDLV	214
GIAFADKYRKT---GG---VVVTTTGDGGSSEGETYEAMNFAKLHEVPC	188
GVALGLKMRGK---KA---VAITYTGDGGSQGDFFYEGINFAGAFKAPA	196

G.AFA.KYR.....-V..T..GDG..NQQ.FE..NMA.LW.LP.	250
--	-----

*3

IFVVENNLWAIGMSHLRATSDPEIWKKGPAFGMPGVHVDGMDVLKVREVA	299
IFVVENNQWAIGMAHHRSSSIPEIHKKAFAFLPGIEVDGMDVLAVRQVA	240
ILVCENNHGGMGTAEWRAAKSPSYKRGD-Y-VPGLKVDGMDAFVAVKQAC	266
IFICENNRHYGMGTASVERAASTDYKRGD-F-IPGLRVDGMDILCVREAT	266
VFCCENNKYGMGTAAARSSAMTEYFKRGQ-Y-IPGLKVNGMDILAVYQAS	286
LYVCENNGYGMGTAAARSSASTDYTRGD-Y-VPGIWVDGMDVLAVRQAV	262
IFVIENNKWAISTARSEQTKSINFAVKGIATGIPSIIVDGNLACIGVF	238
IFVVQNNRFAISTPVEKQTVAKTLAQKAVAAGIPGIQVDGMDPLAVYAAV	246

IFV.ENN....GTA..R.....K.G.....PG..VDGMD.LAV...A.	300
--	-----

*1 . 2

KEAVTRARRGEGPTLVECETYRFRGHSLADPD-ELRDAAE-KAKYAARDP	347
EKAVERARQGQPTLIEALTYRFRGHSLADPD-ELRSRQE-KEAWVARDP	288
KFAKQHALE-KGPIILEMDTYRYHGHSMSPGSTYRTRDEISGVRQERDP	315
RFAAAYCRSGKGPILMELQTYRYHGHSMSPGVSYRTREEIQEVRSKSDP	316
KFAKDWCLSGKGPLVLEYETYRYGGHSMSPGTTYRTRDEIQHMRSKNDP	336
RWAKEWCNAGKGPLMIEMATYRYSGHSMSPGTSYRTREEVQEVKTRDP	312
KEVVEYVRKGNPVLVECDTYRLGAHSSSDNPDAYRPKGEFEEM-AKFDP	287
KAARERAINGEGPTLIETLCFRYGPHTMSGDDPTRYRSKELENEWAKKDP	296

K.A.....G.GP.L.E..TYRY.GHSMSP...YR.R.E.....DP	350
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14/19

FIG. 8C

IAALKKYLIENKLAKEAELKSIEKKIDELVEEAVEFADASPQPG--RSQL	395
IKKLKKHILDNQIASSDELNDIQSSVKIDLEQSVFAMSSPEPN--ISEL	336
IERIKKLVLSHDLATEKELKDMEKEIRKEVDDAIKAKDCPMPE--PSEL	363
IMLLKDRMVNSNLASVEELKEIDVEVRKEIEDAAQFATADPEPP--LEEL	364
IAGLKMHLIDLGIATEAEVKAYDKSARKYVDEQVELADAAPPPEAKLSIL	386
ITGFKDKIVTAGLVTEDEIKEIDKQVRKEIDAAVKQAHTDKESPVELMLT	362
LIRLKQYLIDKKIWSDEQQAQLEAEQDKFVADEFWVEKNKNYDL-IDIF	336
LVRFRKFLEAKGLWSEEEENNVEQAKEEIKEAIKKADETPKQK--VTDL	344
I..LK.....LA.E.E.K.....K....A...A...P.P.---..L	400
LENVFADPKGFGIGPDGRYRCEDPKFTEG-TAQV	428
-----K-----RY-----LFADN-----	344
FTNVYV--KGFG---TESFGPDRKEVKAS-LP--	389
GYHIYSSDPPF----EVRGANQWIKFKSVS----	390
FEDVYVKGTTETPTLRGRI PEDTWDFKKQGFASRD	420
DIYYNTPAQYVRCTTDEVLQKYLTSEEAVKALAK	396
KYQYDKMDIFLEEYQKEAKEFFEKYPESKEGGHH	370
ISIMFE-ELPF-----NLKEQYEIYKEKESK--	369
.....	434

336 363 364 386 362 336 344 400 428 344 389 390 420 396 370 369 434

15/19

GAAMTGLRPVIEGMNMGFLLAFNQISNNCGMLHYTSGGQFTIPVVIRGP	200
GAAITGLRPIVEGMNMSFLLAFNQISNNAGMLRYTSGGNFTLPLVIRGP	118
GAAYAGLKPVVEFMTFNFSMQAIDHIINSAAKSNYMSAGQINVPIVFRGP	150
GAAMAGLRPICEFMTFNFSMQAIDQVINSAAKTYYSGGQLQVPVIVFRGP	147
GAALKGLKPIVEFMSFNFSMQAIDHVVNSAAKTHYMSGGTQKCQMVFRGP	153

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16/19

FIG. 9B

GAAMNGLRPICEFMSMNFMSMQGIDHIINSAAKAHYMSAGR FHVPIVFRGA	148
GMAMNGMKPVLEMQFEGLGLASLQNI FTNISRMNRNTRGKYTAPMVI RMP	118
GLALQGFRPVPEIQFFGFVYEVMD SICQMARIYRTGGRYHMPITIRSP	118
GAA..GLRP..E.M...F...A.D.I.N.AA...Y.SGG....P.V.RGP	200

Region 2

Region 2	
GGVGRQLGAEHSQRLESYFQSIPIGIQMVACSTPYNAKGLMKA AIRSENPV	250
GGVGRQLGAEHSQRLEAYFQAIPLGLKIVACSTPYNAKGLLKS AIRDNNPV	168
NGAAAGVGAQHSQC YAAWYASVPGLKVLAPYSAEDARGLLKAA IRDPDPV	200
NGASAGVAAQHSQCFAAWYGHCPGLKVVSPWNSEDAKGLIKS AIRDNNPV	197
NGAAVGLGAQHSQDFSPWYGSIPGLKVLVPYSAEDARGLLKAA IRDPNPV	203
NGAAVGVAQQHSQDFTAWFMHCPGVKVVVPYDCEDARGLLKAA VRDDNPV	198
MGGGIRALEHHSEALEAVYAHIPGVQIVCPSTPYDTKGLILAA IDS PDPV	168
FGGGVHTPELHSDSLEGLVAQQPGLKVVIPSTPYDAKGLLIS AIRDNDPV	168
.G.....A.HSQ...A.....PGLKVV.P....DAKGLLKAA IRD.NPV	250

ILFEHVLLYN---	LKEKIPDEDYICNLEEAEMVRPGEHITILTYSRMR	296
VFFEHVLLYN---	LQEEIPEDEYLIPLDKAEVVRKGDITILTYSRMRH	214
VFLENELLYGESFPI	SEEALDSSFCLPIGKAKIEREGKDVTVTF SKMVG	250
VVLENELMYGVPFEFL	PEAQSKDFLIPIGKAKIERQGTHITVVS HSRPVG	247
VFLENELLYGESFEI	SEEALSPEFTLPY-KAKIEREGDISIVTYTRNVQ	252
ICLENEIILYGMKFPVS	PEAQSPDFVL PFGQAKIQRPGKDITIVSLSIGVD	248
IVVEPTKLYR---	AFKQEV PDEHYIVPIGEGYKIQEGNDLTVVTVGAQTV	215
IFLEHLKLYR---	SFRQEVPEGEYTIPIGKADIKREGKDITIIAYGAMVH	215
..LE..LLY.....E.....P.GKA.I.R.G.DITIVTYS..V.		300

Region 3

Region 3		
HVMQAAKTLVNK--GYDPEVIDIRSLKPFDLHTIGNSVKKTHRVLIVEEC		344
HVTEALPLLLND--GYDPEVLDLISLPLDIDSISVSVKKTHRVLIVEEC		262
FALKAAEKLAAE--GISAEVINLRSIRPLDRATINASVRKTSRLVTVEEG		298
HCLEAAAVLSKE--GVECEVINMRTIRPDMETIEASVMKTNHLVTVEGG		295
FSLEAAEILQKKY-GVSAEVINLRSIRPLDEAI IKTVKTNHLLITVEST		301
VSLHAADELAKS--GIDCEVINLRCVRPLDFQTVKDSVIKTKHLVTVESG		296
DCQKAIALLKETHPNATIDLIDLRSIKPWDKKMVIESVKKTGRLLVHEA		265
ESLKAAAELEKE--GISAEVVDLRTVQPLDIETIIGSVEKTGRAIVVQEA		263
...L.AA..L....-G...EVI.LRS..PLD..TI..SV.KT.RL..VEE.		350

Region 4

MR TGGIGASLTAAINE-NFHDYLDAPVMCLSSQDVPTPYAGTLEEWTVVQ 393

18/19

A. t.	MAA-----LLG-RSC-----RKLSFPSLTHG-----ARR-	23
Human	MAVVAAGGWLRLRLRAAGAEHWRRLPGAGLARGFLHPAATVEDAAQRRQ	50
Bovine	MAVAAGFAGWLRLRLRAAGADGPWRRLCGAGLSRGFLQSASAY-GAAQRRQ	49
Consensus	MAVAAGGWLRLRLRAAGAGWRRLGAGLRGFLA...AAQRRQ	50

V-----STETGKP--LNLYSAINQALHIALDTPRSYVFGE	61
VAHFTFQPDPEPREYGTQKMNLFQSVTSALDNSLAKDPTAVIFGEDVAF	100
VAHFTFQPDPEPVEYGTQKMNLFQAVTSALDNSLAKDPTAVIFGEDVAF	99
VAHFTFQPDPEP.EYGTQKMNLFQAVTSALDNSLAKDPTAVIFGEDVAF	100

GGVFRCTTGLAERFGKNRVFNTPLCEQGIVGFGIGLAAMGNRAIVEIQFA	111
GGVFRCTVGLRDKY GKDRVFNTPLCEQGIVGFGIGIAVTGATAIAEIQFA	150
GGVFRCTVGLRDKY GKDRVFNTPLCEQGIVGFGIGIAVTGATAIAEIQFA	149
GGVFRCTVGLRDKY GKDRVFNTPLCEQGIVGFGIGIAVTGATAIAEIQFA	150

DYIYPAFDQIVNEAAKFRYRSGNQFNCGGLTIRAPYGAVGHGGHYHSQSP	161
DYIFPAFDQIVNEAAKYRYRSGDLFNCGSLTIRSPWGCVGHGALYHSQSP	200
DYIFPAFDQIVNEAAKYRYRSGDLFNCGSLTIRSPWGCVGHGALYHSQSP	199
DYIFPAFDQIVNEAAKYRYRSGDLFNCGSLTIRSPWGCVGHGALYHSQSP	200

EAF FCHVPGIKVVI PRSPREAKG LLLSCIRDPNPVVF FE PKWLYRQAVEE	211
EAF FAHCPGIK VVI PRSPFQAKG LLLSCIEDKNPCIFFE PKILYRAAAEE	250
EAF FAHCPGIK VVV PRSPFQAKG LLLSCIEDKNPCIFFE PKILYRAAVEQ	249
EAF FAHCPGIK VVI PRSPFQAKG LLLSCIEDKNPCIFFE PKILYRAAVEE	250

